

SEQUENCE LISTING

<110> Tanuma, Sei-ichi
 Shiokawa, Daisuke
 <120> Novel Deoxyribonuclease, Gene Encoding Thereof and Use Thereof
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 <151> 1999-08-17
 <150> US 09/807,784
 <151> 2001-04-17
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 45 50 55
 Ser Ala Leu Gly Arg Thr Leu Gln His Leu Tyr Asp Thr His Asn Ser
 60 65 70
 Thr Asn Asp Thr Ala Tyr Leu Ile Tyr Asn Asp Gly Val Pro Gly Ser
 75 80 85 90
 Val Asn Tyr Ser Arg Gln Tyr Gly His Ala Lys Gly Leu Leu Val Trp
 95 100 105
 Asn Arg Thr Gln Gly Phe Trp Leu Ile His Ser Val Pro Lys Phe Pro
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 Pro Val His Gly Tyr Glu Tyr Pro Thr Ser Gly Arg Arg Tyr Gly Gln
 125 130 135
 Thr Gly Ile Cys Ile Thr Phe Gly Tyr Ser Gln Phe Glu Glu Ile Asp
 140 145 150
 Phe Gln Leu Leu Val Leu Gln Pro Asn Ile Tyr Ser Cys Phe Ile Pro
 155 160 165 170
 Ser Thr Phe His Trp Lys Leu Ile Tyr Met Pro Arg Met Cys Ala Asn
 175 180 185
 Ser Ser Ser Leu Lys Ile Pro Val Arg Tyr Leu Ala Glu Leu His Ser
 190 195 200
 Ala Gln Gly Leu Asn Phe Val His Phe Ala Lys Ser Ser Phe Tyr Thr
 205 210 215

224589.ST25

Asp Asp Ile Phe Thr Gly Trp Ile Ala Gln Lys Leu Lys Thr His Leu
 220 225 230
 Leu Ala Gln Thr Trp Gln Lys Lys Lys Gln Glu Leu Pro Ser Asn Cys
 235 240 245 250
 Ser Leu Pro Tyr His Val Tyr Asn Ile Lys Ser Ile Gly Val Thr Ser
 255 260 265
 Lys Ser Tyr Phe Ser Ser Arg Gln Asp His Ser Lys Trp Cys Val Ser
 270 275 280
 Ile Lys Gly Ser Ala Asn Arg Trp Thr Cys Ile Gly Asp Leu Asn Arg
 285 290 295
 Ser Leu His Gln Ala Leu Arg Gly Gly Gly Phe Ile Cys Thr Lys Asn
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<220>
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 aaccgacccg caagggagcc aacgcggcct gagaaagacc tgacactctg actccacagt 180
 cccctgcatg gaatgaaggc cacagataga aa atg aca gca aag cct cta aga 233
 Met Thr Ala Lys Pro Leu Arg
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 aca gtt ctt tct ttg ctc ttc ttt gcc ctc tct ggg gtc ctg ggg aca 281
 Thr Val Leu Ser Leu Phe Phe Ala Leu Ser Gly Val Leu Gly Thr 1
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 Pro Glu Ile Ser Cys Arg Asn Glu Tyr Gly Glu Ala Val Asp Trp Phe 5 10 15
 atc ttt tat aag tta ccc aaa agg act agc aag gca agt gaa gag gcg 377
 Ile Phe Tyr Lys Leu Pro Lys Arg Thr Ser Lys Ala Ser Glu Glu Ala 20 25 30
 ggg ctg cag tac ctg tac ctg gac tcc aca aga caa acc tgg aac aag 425
 Gly Leu Gln Tyr Leu Tyr Leu Asp Ser Thr Arg Gln Thr Trp Asn Lys 35 40 45
 agc ctc tac ctg att aac agc acc agg agt gct ctg ggg agg acc tta 473
 Ser Leu Tyr Leu Ile Asn Ser Thr Arg Ser Ala Leu Gly Arg Thr Leu 50 55 60 65
 cag cat ctg tat gac aca cat aat tcc acg aat gac aca gcc tat cta 521
 Gln His Leu Tyr Asp Thr His Asn Ser Thr Asn Asp Thr Ala Tyr Leu 70 75 80
 ata tac aac gat ggt gtc cct gga tct gtg aat tac agc aga cag tat 569
 Ile Tyr Asn Asp Gly Val Pro Gly Ser Val Asn Tyr Ser Arg Gln Tyr 85 90 95

224589.ST25

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Gly	His	Ala	Lys	Gly	Leu	Leu	Val	Trp	Asn	Arg	Thr	Gln	Gly	Phe	Trp						
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ctg	ata	cac	tct	ggt	ccc	aag	ttt	ccc	cca	ggt	cat	ggc	tat	gag	tac	665					
Leu	Ile	His	Ser	Val	Pro	Lys	Phe	Pro	Pro	Val	His	Gly	Tyr	Glu	Tyr						
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cca	acc	tgc	ggg	agg	cga	tat	gga	caa	acc	ggc	atc	tgc	atc	act	ttc	713					
Pro	Thr	Ser	Gly	Arg	Arg	Tyr	Gly	Gln	Thr	Gly	Ile	Cys	Ile	Thr	Phe						
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Gly	Tyr	Ser	Gln	Phe	Glu	Glu	Ile	Asp	Phe	Gln	Leu	Leu	Val	Leu	Gln						
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Pro	Asn	Ile	Tyr	Ser	Cys	Phe	Ile	Pro	Ser	Thr	Phe	His	Trp	Lys	Leu						
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Ile	Tyr	Met	Pro	Arg	Met	Cys	Ala	Asn	Ser	Ser	Ser	Leu	Lys	Ile	Pro						
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gtc	cgg	tac	ctc	gct	gaa	ctg	cac	tca	gcc	cag	ggt	cta	aac	ttc	gtc	905					
Val	Arg	Tyr	Leu	Ala	Glu	Leu	His	Ser	Ala	Gln	Gly	Leu	Asn	Phe	Val						
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Lys	Lys	Gln	Glu	Leu	Pro	Ser	Asn	Cys	Ser	Leu	Pro	Tyr	His	Val	Tyr						
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Asn	Ile	Lys	Ser	Ile	Gly	Val	Thr	Ser	Lys	Ser	Tyr	Phe	Ser	Ser	Arg						
		260					265					270									
caa	gac	cat	tcc	aaa	tgg	tgt	ggt	tcc	ata	aag	ggc	tcc	gca	aat	cgc	1145					
Gln	Asp	His	Ser	Lys	Trp	Cys	Val	Ser	Ile	Lys	Gly	Ser	Ala	Asn	Arg						
	275					280					285										
tgg	acc	tgc	att	gga	gac	cta	aat	cga	agc	cta	cac	caa	gcc	tta	aga	1193					
Trp	Thr	Cys	Ile	Gly	Asp	Leu	Asn	Arg	Ser	Leu	His	Gln	Ala	Leu	Arg						
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Gly	Gly	Gly	Phe	Ile	Cys	Thr	Lys	Asn	His	Tyr	Ile	Tyr	Gln	Ala	Phe						
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224589.ST25

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 <213> Homo sapiens

<400> 3

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 Pro Lys Arg Gln Asn Lys Glu Ser Gly Glu Thr Gly Leu Glu Tyr Leu
 25 30 35
 Tyr Leu Asp Ser Thr Thr Arg Ser Trp Arg Lys Ser Glu Gln Leu Met
 40 45 50
 Asn Asp Thr Lys Ser Val Leu Gly Arg Thr Leu Gln Gln Leu Tyr Glu
 55 60 65
 Ala Tyr Ala Ser Lys Ser Asn Asn Thr Ala Tyr Leu Ile Tyr Asn Asp
 70 75 80 85
 Gly Val Pro Lys Pro Val Asn Tyr Ser Arg Lys Tyr Gly His Thr Lys
 90 95 100
 Gly Leu Leu Leu Trp Asn Arg Val Gln Gly Phe Trp Leu Ile His Ser
 105 110 115
 Ile Pro Gln Phe Pro Pro Ile Pro Glu Glu Gly Tyr Asp Tyr Pro Pro
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 Thr Gly Arg Arg Asn Gly Gln Ser Gly Ile Cys Ile Thr Phe Lys Tyr
 135 140 145
 Asn Gln Tyr Glu Ala Ile Asp Ser Gln Leu Leu Val Cys Asn Pro Asn
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 Val Tyr Ser Cys Ser Ile Pro Ala Thr Phe His Gln Glu Leu Ile His
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 Met Pro Gln Leu Cys Thr Arg Ala Ser Ser Ser Glu Ile Pro Gly Arg
 185 190 195
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 Ala Lys Ser Asp Ser Phe Leu Asp Gly Ile Phe Ala Ala Trp Met Ala
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 Gln Arg Leu Lys Thr His Leu Leu Thr Glu Thr Trp Gln Arg Lys Arg
 230 235 240 245
 Gln Glu Leu Pro Ser Asn Cys Ser Leu Pro Tyr His Val Tyr Asn Ile
 250 255 260
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 265 270 275
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 280 285 290
 Cys Ile Gly Asp Leu Asn Arg Ser Pro His Gln Ala Phe Arg Ser Gly

224589.ST25
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295

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Leu Phe Leu Gly Leu Phe Gly Val Leu Gly Ala Ala Thr Ile Ser Cys
-10 -5 1 5
aga aat gaa gaa ggg aaa gct gtg gac tgg ttt act ttt tat aag tta 144
Arg Asn Glu Glu Gly Lys Ala Val Asp Trp Phe Thr Phe Tyr Lys Leu
10 15 20
cct aaa aga caa aac aag gaa agt gga gag act ggg tta gag tac ctg 192
Pro Lys Arg Gln Asn Lys Glu Ser Gly Glu Thr Gly Leu Glu Tyr Leu
25 30 35
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Tyr Leu Asp Ser Thr Thr Arg Ser Trp Arg Lys Ser Glu Gln Leu Met
40 45 50
aat gac acc aag agt gtt ttg gga agg aca tta caa cag cta tat gaa 288
Asn Asp Thr Lys Ser Val Leu Gly Arg Thr Leu Gln Gln Leu Tyr Glu
55 60 65
gca tat gcc tct aag agt aac aac aca gcc tat cta ata tac aat gat 336
Ala Tyr Ala Ser Lys Ser Asn Asn Thr Ala Tyr Leu Ile Tyr Asn Asp
70 75 80 85
gga gtc cct aaa cct gtg aat tac agc aga aag tat gga cac acc aaa 384
Gly Val Pro Lys Pro Val Asn Tyr Ser Arg Lys Tyr Gly His Thr Lys
90 95 100
ggt tta ctg ctg tgg aac aga gtt caa ggg ttc tgg ctg att cat tcc 432
Gly Leu Leu Leu Trp Asn Arg Val Gln Gly Phe Trp Leu Ile His Ser
105 110 115
atc cct cag ttt cct cca att ccg gaa gaa ggc tat gat tat cca ccc 480
Ile Pro Gln Phe Pro Pro Ile Pro Glu Glu Gly Tyr Asp Tyr Pro Pro
120 125 130
aca ggg aga cga aat gga caa agt ggc atc tgc ata act ttc aag tac 528
Thr Gly Arg Arg Asn Gly Gln Ser Gly Ile Cys Ile Thr Phe Lys Tyr
135 140 145
aac cag tat gag gca ata gat tct cag ctc ttg gtc tgc aac ccc aac 576
Asn Gln Tyr Glu Ala Ile Asp Ser Gln Leu Val Cys Asn Pro Asn
150 155 160 165
gtc tat agc tgc tcc atc cca gcc acc ttt cac cag gag ctc att cac 624

224589.ST25

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Met	Pro	Gln	Leu	Cys	Thr	Arg	Ala	Ser	Ser	Ser	Glu	Ile	Pro	Gly	Arg	
			185					190					195			
ctc	ctc	acc	aca	ctt	cag	tcg	gcc	cag	gga	caa	aaa	ttc	ctc	cat	ttt	720
Leu	Leu	Thr	Thr	Leu	Gln	Ser	Ala	Gln	Gly	Gln	Lys	Phe	Leu	His	Phe	
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Gln	Arg	Leu	Lys	Thr	His	Leu	Leu	Thr	Glu	Thr	Trp	Gln	Arg	Lys	Arg	
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caa	gag	ctt	cct	tca	aac	tgc	tcc	ctt	cct	tac	cat	gtc	tac	aat	ata	864
Gln	Glu	Leu	Pro	Ser	Asn	Cys	Ser	Leu	Pro	Tyr	His	Val	Tyr	Asn	Ile	
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aaa	gca	att	aaa	tta	tca	cga	cac	tct	tat	ttc	agt	tct	tat	caa	gat	912
Lys	Ala	Ile	Lys	Leu	Ser	Arg	His	Ser	Tyr	Phe	Ser	Ser	Tyr	Gln	Asp	
			265					270					275			
cat	gcc	aag	tgg	tgt	att	tcc	caa	aag	ggc	acc	aaa	aat	cgc	tgg	aca	960
His	Ala	Lys	Trp	Cys	Ile	Ser	Gln	Lys	Gly	Thr	Lys	Asn	Arg	Trp	Thr	
		280					285					290				
tgt	att	gga	gac	cta	aat	cgg	agt	cca	cac	caa	gcc	ttc	aga	agt	gga	1008
Cys	Ile	Gly	Asp	Leu	Asn	Arg	Ser	Pro	His	Gln	Ala	Phe	Arg	Ser	Gly	
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gga	ttc	att	tgt	acc	cag	aat	tgg	caa	att	tac	caa	gca	ttt	caa	gga	1056
Gly	Phe	Ile	Cys	Thr	Gln	Asn	Trp	Gln	Ile	Tyr	Gln	Ala	Phe	Gln	Gly	
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tta	gta	tta	tac	tat	gaa	agc	tgt	aag	taa							1086
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<220>
 <223> oligonucleotide designed to act as sense primer for amplifying 3'-terminal of mouse DLAD cDNA.

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<210> 6
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide designed to act as antisense primer for amplifying 5'-terminal of mouse DLAD cDNA.

<400> 6
 ccatcgttgt atattagata ggctgtg 27

224589.ST25

<210> 7
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide designed to act as linker primer for
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<400> 7
 ccacccaat acgactcact atagggc

27

<210> 8
 <211> 52
 <212> DNA
 <213> Artificial Sequence

<220>
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 <222> (51)..(51)
 <223> "v" is g, a or c.

<220>
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 <222> (52)..(52)
 <223> "n" is g, a, c or t.

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 <213> Artificial Sequence

<220>
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35

<210> 10
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 <213> Artificial Sequence

<220>
 <223> oligonucleotide designed to act as antisense primer for
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<400> 10
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30

<210> 11
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
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<210> 12
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide designed to act as antisense primer for
 amplifying coding sequence of DNase II signal peptide.

<400> 12
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<210> 13
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide designed to act as sense primer for
 amplifying coding sequence of DLAD lacking its signal peptide.

<400> 13
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<210> 14
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide designed to act as sense primer for
 amplifying 3'-terminal of human DLAD cDNA.

<400> 14
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<210> 15
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide designed to act as antisense primer for
 amplifying 5'-terminal of human DLAD cDNA.

<400> 15
 gaaggcttgg tgtggactcc gatttag 27